IN THE CLAIMS:

The text of all pending claims, (including withdrawn claims) is set forth below. Cancelled and not entered claims are indicated with claim number and status only. The claims as listed below show added text with <u>underlining</u> and deleted text with ~~strikethrough~~. The status of each claim is indicated with one of (original), (currently amended), (cancelled), (withdrawn), (new), (previously presented), or (not entered).

Please CANCEL without prejudice or disclaimer claims 1-24 the underlying PCT application and ADD new claims 25-47 in accordance with the following:

Claims 1-24 (Cancelled)

25. (New) A method for analysis of a regulatory genetic network of a cell using a causal network describing a regulatory genetic network of cells such that nodes of the causal network represent genes of the regulatory genetic network and connectors of the causal networks represent regulatory interactions between the genes of the regulatory genetic network, said method comprising:

providing a predetermined gene expression rate for a selected gene of the regulatory genetic network;

generating a resulting gene expression pattern for the regulatory genetic network using the causal network for the predetermined gene expression rate; and

comparing the resulting gene expression pattern with a predetermined gene expression pattern of the regulatory genetic network.

26. (New) A method in accordance with claim 25, further comprising selecting the selected gene by dependency analysis using the causal network.

27. (New) A method in accordance with claim 26, wherein the predetermined gene expression rate of the selected gene reflects an assumption of a gene defect.

28. (New) A method in accordance with claim 27, wherein the causal network is a Bayesian network.

29. (New) A method in accordance with claim 28, wherein the causal network is a directed acylic graph type.

30. (New) A method in accordance with claim 29, wherein at least one of the resulting gene expression pattern and the predetermined gene expression pattern represents discrete gene states.

31. (New) A method in accordance with claim 30, wherein the discrete gene states include an overexpressed gene state, a normally expressed gene state and an underexpressed gene state.

32. (New) A method in accordance with claim 31, wherein said comparing of the resulting gene expression pattern to the predetermined gene expression pattern uses at least one of a static method and a statistical code as a measure of distance.

33. (New) A method in accordance with claim 32, further comprising training the causal network using training gene expression patterns to adapt the nodes and the connectors of the causal network.

34. (New) A method in accordance with claim 33, further comprising determining at least one of the predetermined gene expression pattern and the training gene expression patterns using a DNA microarray technique.

35. (New) A method in accordance with claim 34, wherein at least one of the predetermined gene expression pattern and the training gene expression patterns are for a diseased cell.

36. (New) A method in accordance with claim 35, wherein the diseased cell is an oncocell.

37. (New) A method in accordance with claim 36, wherein the diseased cell features an Acute Lymphoblastic Leukemia oncogene.

38. (New) A method in accordance with claim 25, further comprising repeating said determining, said generating and said comparing to determine a plurality of predetermined gene expression rates for selected genes of the regulatory genetic network and to generate and compare the resulting gene expression pattern for each of the predetermined gene expression rates with a corresponding predetermined gene expression pattern.

39. (New) A method in accordance with claim 38, wherein said repeating of the generation the resulting gene expression patterns is performed iteratively.

40. (New) A method in accordance with claim 39, further comprising identifying a dominant gene based on said comparing repeatedly performed.

41. (New) A method in accordance with claim 39, further comprising identifying at least one of a degenerated gene, a mutated gene, a diseased gene, an oncogene, and a tumor-suppressor gene based on said comparing repeatedly performed.

42. (New) A method in accordance with claim 39, further comprising identifying a tumor cell based on said comparing repeatedly performed.

43. (New) A method in accordance with claim 39, further comprising detecting cancer based on said comparing repeatedly performed.

44. (New) A method in accordance with claim 39, further comprising analyzing a cause of an abnormal gene expression pattern/gene expression rate based on said comparing repeatedly performed.

45. (New) A method in accordance with claim 39, further comprising simulating an effect of a medicament based on said comparing repeatedly performed.

46. (New) A method in accordance with claim 39, further comprising analyzing an effect of a medicament based on said comparing repeatedly performed.

47. (New) At least one computer-readable medium storing a program which when executed on a computer causes the computer to perform a method comprising:

providing a predetermined gene expression rate for a selected gene of the regulatory genetic network;

generating a resulting gene expression pattern for the regulatory genetic network using the causal network for the predetermined gene expression rate; and

comparing the generated resulting gene expression pattern with a predetermined gene expression pattern of the regulatory genetic network.